

AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

Claims 1-59. (Canceled)

60. (new) A method of genotyping HCV nucleic acids present in a biological sample comprising the steps of

contacting nucleic acids of the 5' UTR of HCV in a biological sample with multiple oligonucleotide probes under reaction conditions in which said probes specifically hybridize to target sequences in said HCV 5' UTR nucleic acids within the region extending from the nucleotides at positions -291 to -66, if present in the biological sample, and

determining whether one or more of said probes have hybridized to said nucleic acids of HCV,

wherein, under said reaction conditions, said probes can distinguish among at least three genotypes of HCV selected from the group consisting of HCV type 1, HCV type 2, HCV type 3, and HCV type 4, and classify the HCV nucleic acids into any of said at least three genotypes, if any of said at least three genotypes is present in said sample.

61. (new) The method according to claim 60, wherein said multiple probes can distinguish among four genotypes of HCV selected from the group consisting of HCV type 1, HCV type 2, HCV type 3, and HCV type 4, and classify the HCV nucleic acids present in said sample into any of HCV type 1, HCV type 2, HCV type 3 or HCV type 4, if any of said genotypes is present in said sample.

62. (new) A method of genotyping HCV nucleic acids present in a biological sample comprising the steps of

contacting nucleic acids of the 5' UTR of HCV in a biological sample with multiple oligonucleotide probes under reaction conditions in which said probes specifically hybridize to target sequences in said HCV 5' UTR nucleic acids within the region extending from the nucleotides at positions -291 to -66, if present in the biological sample, and

determining whether one or more of said probes have hybridized to said nucleic acids of HCV,

wherein, under said reaction conditions, said probes can distinguish among at least three genotypes of HCV selected from the group consisting of HCV type 1, HCV type 2, HCV type 3, HCV type 4, HCV type 5 and HCV type 6, and classify the HCV nucleic acids into any of said at least three genotypes, if any of said at least three genotypes is present in said sample.

63. (new) The method according to claim 62, wherein said multiple probes can distinguish among at least four genotypes of HCV selected from the group consisting of HCV type 1, HCV type 2, HCV type 3, HCV Type 4, HCV type 5 and HCV type 6, and classify the HCV nucleic acids present in said sample into any of said at least four of said genotypes of HCV, if any of said at least four genotypes is present in said sample.

64. (new) The method according to claim 62, wherein said multiple probes can distinguish among at least five genotypes of HCV selected from the group consisting of

HCV type 1, HCV type 2, HCV type 3, HCV Type 4, HCV type 5 and HCV type 6, and classify the HCV nucleic acids present in said sample into any of said at least five genotypes of HCV, if any of said at least five genotypes is present in said sample.

65. (new) The method according to claim 62, wherein said multiple probes can distinguish among six genotypes of HCV selected from the group consisting of HCV type 1, HCV type 2, HCV type 3, HCV Type 4, HCV type 5 and HCV type 6, and classify the HCV nucleic acids present in said sample into any of said six genotypes of HCV, if any of said six genotypes is present in said sample.

66. (new) The method according to any of claims 60-65, wherein said HCV nucleic acids are DNA.

67. (new) The method according to any of claims 60-65, wherein said determining step comprises detecting fluorescence.

68. (new) The method according to any of claims 60-65, wherein said probes are completely homologous to said target sequences.

69. (new) The method according to any of claims 60-65, wherein said probes are not completely homologous to said target sequences.

70. (new) The method according to any of claims 60-65, wherein at least two of

said probes are used at the same time and under the same reaction conditions.

71. (new) The method according to any of claims 60-65, wherein at least three of said probes are used at the same time and under the same reaction conditions.

72. (new) The method according to any of claims 60-65, wherein at least four of said probes are used at the same time and under the same reaction conditions.

73. (new) The method according to any of claims 60-65, wherein at least five of said probes are used at the same time and under the same reaction conditions.

74. (new) The method according to any of claims 60-65, wherein said multiple probes also can distinguish among and classify the HCV nucleic acids into at least two subtypes of HCV, if any of said subtypes are present in said sample.

75. (new) The method according to claim 74, wherein said at least two subtypes of HCV are selected from the group consisting of subtypes 1a, 1b, 2a, 2b, 2c, 3a, 3b, 4a and 4b.

76. (new) The method according to any of claims 60-65, wherein said multiple probes also can distinguish among at least three subtypes of said genotypes of HCV, if any of said subtypes are present in said sample.

77. (new) The method according to claim 76, wherein said at least three subtypes of HCV are selected from the group consisting of subtypes 1a, 1b, 2a, 2b, 3a, 3b, 4a and 4b.

78. (new) The method according to any of claims 60-65, wherein said multiple probes also can distinguish among at least four subtypes of said genotypes of HCV, if said subtypes are present in said sample.

79. (new) The method according to claim 78, wherein said at least four subtypes of HCV are selected from the group consisting of subtypes 1a, 1b, 2a, 2b, 3a, 3b, 4a and 4b.

80. (new) The method according to claim 78, wherein said at least four subtypes of HCV are selected from the group consisting of subtypes 1a, 1b, 2a, 2b, 2c, 3a, 3b, 3c, 4a, 4b, 4c, 4d, 4e, 4f, 4g, and 4h.

81. (new) The method according to any of claims 60-65, wherein at least two of said probes specifically hybridize to genotype-specific target sequences, if present in the biological sample, wherein said genotype-specific target sequences are located in one or more domains selected from the group consisting of:

(a) the one extending from nucleotide at position -291 to nucleotide at position -278,

- (b) the one extending from nucleotide at position -275 to nucleotide at position -260,
- (c) the one extending from nucleotide at position -253 to nucleotide at position -238,
- (d) the one extending from nucleotide at position -244 to nucleotide at position -229,
- (e) the one extending from nucleotide at position -238 to nucleotide at position -223,
- (f) the one extending from nucleotide at position -170 to nucleotide at position -155,
- (g) the one extending from nucleotide at position -141 to nucleotide at position -117,
- (h) the one extending from nucleotide at position -83 to nucleotide at position -68,
- (i) the one extending from nucleotide at position -103 to nucleotide at position -88,
- (j) the one extending from nucleotide at position -146 to nucleotide at position -130.

82. (new) The method according to any of claims 60-65, wherein at least three of said probes specifically hybridize to genotype-specific target sequences, if present in the biological sample, wherein said genotype-specific target sequences are located in one or more domains selected from the group consisting of:

- (a) the one extending from nucleotide at position -291 to nucleotide at position -278,
- (b) the one extending from nucleotide at position -275 to nucleotide at position -260,
- (c) the one extending from nucleotide at position -253 to nucleotide at position -238,
- (d) the one extending from nucleotide at position -244 to nucleotide at position -229,
- (e) the one extending from nucleotide at position -238 to nucleotide at position -223,
- (f) the one extending from nucleotide at position -170 to nucleotide at position -155,
- (g) the one extending from nucleotide at position -141 to nucleotide at position -117,
- (h) the one extending from nucleotide at position -83 to nucleotide at position -68,
- (i) the one extending from nucleotide at position -103 to nucleotide at position -88,
- (j) the one extending from nucleotide at position -146 to nucleotide at position -130.

83. (new) The method according to any of claims 60-65, wherein at least four of

said probes specifically hybridize to genotype-specific target sequences, if present in the biological sample, wherein said genotype-specific target sequences are located in one or more domains selected from the group consisting of:

- (a) the one extending from nucleotide at position -291 to nucleotide at position -278,
- (b) the one extending from nucleotide at position -275 to nucleotide at position -260,
- (c) the one extending from nucleotide at position -253 to nucleotide at position -238,
- (d) the one extending from nucleotide at position -244 to nucleotide at position -229,
- (e) the one extending from nucleotide at position -238 to nucleotide at position -223,
- (f) the one extending from nucleotide at position -170 to nucleotide at position -155,
- (g) the one extending from nucleotide at position -141 to nucleotide at position -117,
- (h) the one extending from nucleotide at position -83 to nucleotide at position -68,
- (i) the one extending from nucleotide at position -103 to nucleotide at position -88,

(j) the one extending from nucleotide at position -146 to nucleotide at position -130.

84. (new) The method according to any of claims 60-65, wherein at least six of said probes specifically hybridize to genotype-specific target sequences, if present in the biological sample, wherein said genotype-specific target sequences are located in one or more domains selected from the group consisting of:

(a) the one extending from nucleotide at position -291 to nucleotide at position -278,

(b) the one extending from nucleotide at position -275 to nucleotide at position -260,

(c) the one extending from nucleotide at position -253 to nucleotide at position -238,

(d) the one extending from nucleotide at position -244 to nucleotide at position -229,

(e) the one extending from nucleotide at position -238 to nucleotide at position -223,

(f) the one extending from nucleotide at position -170 to nucleotide at position -155,

(g) the one extending from nucleotide at position -141 to nucleotide at position -117,

(h) the one extending from nucleotide at position -83 to nucleotide at position -68,

- (i) the one extending from nucleotide at position -103 to nucleotide at position -88,
- (j) the one extending from nucleotide at position -146 to nucleotide at position -130.

85 (new) A method of genotyping HCV Type 6 nucleic acids present in a biological sample comprising the steps of:

contacting a biological sample comprising nucleic acids of the 5' UTR of HCV Type 6 with at least one probe, and

determining whether said at least one probe has hybridized to said nucleic acids of HCV,

wherein said step of contacting is carried out under reaction conditions in which said at least one probe specifically hybridizes to a HCV type 6 specific sequence in the 5' UTR, if said HCV type 6 specific sequence in the 5' UTR is present in the biological sample.

86. (new) A method according to claim 85, wherein the at least one probe specifically hybridizes under the reaction conditions to the domain of:

GGG TCC TTT CCA TTG G (SEQ ID NO:48)

or a domain fully complementary to the above sequence.